

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Levy, Gary
- (ii) TITLE OF INVENTION: Methods of Modulating Immune Coagulation
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: BERESKIN & PARR
  - (B) STREET: 40 King Street West
  - (C) CITY: Toronto
  - (D) STATE: Ontario
  - (E) COUNTRY: Canada
  - (F) ZIP: M5H 3Y3
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Gravelle, Micheline
  - (B) REGISTRATION NUMBER: 40,261
  - (C) REFERENCE/DOCKET NUMBER: 9579-006
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (416) 364-7311
  - (B) TELEFAX: (416) 361-1398

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4630 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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 AAGAGCAAAG GATGTCTGCC CAGTGAGACT AGAAAGCAGA GGGAAATGCG AAGAGGCAGG 1500  
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 AGAGAGTGAG GTTAACAAGC TGTCCTCTGA GCTAAAGAAT GCCAAAGAGG AGATCAATGT 1800  
 ACTTCATGGT CGCCTGGAGA AGCTGAATCT TGTAATATG AACAACATAG AAAATTATGT 1860  
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 TTACAATTCT TTTAATTTCT ATTGAACTT TTTCTATTGC TTGTATTACT TGCTGTATTT 3420  
 AAAAAATAAT TGTTGGCTGG GTGTGGTAGC TCACGCCTGT AATCCCAGCA CTTTGGAATG 3480  
 TCAAGGCAGG CAGATCACTT GAGGTCAGGA GTTTGAGACC AGCCTGGCCA AACATGTGAA 3540  
 ACGCTGTCTC TATTAATAAT ACAAATAA GCCGGGCATG GTGGTACATG CCTGTAATCA 3600  
 ACGCTGTTTA TTAATAATAC AAAAATTAGC CGGGCATGGT GGACATGCCT GTAATCCTAG 3660  
 TACTTGGGAG GCTGAGGCAG GAGAATCGCT TGAACCTGAG AGGAAGAGGT TGCAGTGAGC 3720  
 CAAGAATGAG CCACTGCACT CCAGCATGGG TGACAGAGAA AACTCTGTCT CAAACAAAAA 3780  
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 AGTAGTTAAA ATACTATATA TTTCAACCCT GGCTGGTAGA TTGCTTATTT TACTATCAGA 4500  
 AACTAAAAGA TAGATTTTTC CCCAAACAGA AGTATCTGTA ATTTTATATA TTCATCAATT 4560  
 CTGGAATGCT ATATATAATA TTTAAAAGAC TTTTAAATG TGTTTAATTT CATCATCGTA 4620  
 AAAAGGGATC 4630

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Leu Ala Asn Trp Tyr Trp Leu Ser Ser Ala Val Leu Ala Thr  
 1 5 10 15  
 Tyr Gly Phe Leu Val Val Ala Asn Asn Glu Thr Glu Glu Ile Lys Asp  
 20 25 30  
 Glu Arg Ala Lys Asp Val Cys Pro Val Arg Leu Glu Ser Arg Gly Lys  
 35 40 45  
 Cys Glu Glu Ala Gly Glu Cys Pro Tyr Gln Val Ser Leu Pro Pro Leu  
 50 55 60  
 Thr Ile Gln Leu Pro Lys Gln Phe Ser Arg Ile Glu Glu Val Phe Lys  
 65 70 75 80  
 Glu Val Gln Asn Leu Lys Glu Ile Val Asn Ser Leu Lys Lys Ser Cys  
 85 90 95  
 Gln Asp Cys Lys Leu Gln Ala Asp Asp Asn Gly Asp Pro Gly Arg Asn  
 100 105 110  
 Gly Leu Leu Leu Pro Ser Thr Gly Ala Pro Gly Glu Val Gly Asp Asn  
 115 120 125  
 Arg Val Arg Glu Leu Glu Ser Glu Val Asn Lys Leu Ser Ser Glu Leu  
 130 135 140  
 Lys Asn Ala Lys Glu Glu Ile Asn Val Leu His Gly Arg Leu Glu Lys  
 145 150 155 160  
 Leu Asn Leu Val Asn Met Asn Asn Ile Glu Asn Tyr Val Asp Ser Lys  
 165 170 175  
 Val Ala Asn Leu Thr Phe Val Val Asn Ser Leu Asp Gly Lys Cys Ser  
 180 185 190  
 Lys Cys Pro Ser Gln Glu Gln Ile Gln Ser Arg Pro Val Gln His Leu  
 195 200 205  
 Ile Tyr Lys Asp Cys Ser Asp Tyr Tyr Ala Ile Gly Lys Arg Ser Ser  
 210 215 220

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(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: other nucleic acid

CATAAGGCGT	GTCTGACAAA	TTCTTCATAC	ACACATTTCC	CCTTTGCACA	TTCAGTCTGT	60
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TGAAGGCTCA	GCAAAGCCAA	TACGTGTTAT	GTCCAGTTGG	AGACAGTGCC	AGGGCCAACA	180
TTCCAGACTT	CTCAGATAGA	AAGTGC GCCT	GCCTGCCCTG	CTCTGAGAAT	TTGAAGAGAG	240
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CAGCCACTGC	CTGTGATGTG	TGAGTGACGT	GCTTCCAAGT	GTTTTAACCA	CTGACGATTA	660
CATAGCCTGC	ACAGTCAGGA	GAAAACAGCC	GTATTCTCTG	CCAGTTCTCT	TCCCTTTTAC	720
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CCCCAACTAG	GGAGGAAACA	GAATCATTTT	CATTTTGGTG	ACATTTAGTG	GGAAGAAGCT	900
CACAGACATT	TAGACGTTCC	AACTCTTTCC	CCACTAGTGG	ACCAAGTATA	TAATATGGTA	960
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CAGAACGCCT	GAGTCAGGCG	GCGGTGGCTA	TTAAAGCGCC	TGGTCAGGCT	GGGCTGCCGC	1260
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ACCCTGCCCA	CGCTGACCAT	CCAGCTCCCG	CGGCAGCTTG	GCAGCATGGA	GGAGGTGCTC	1500
AAAGAAGTGC	GGACCCTCAA	GGAAGCAGTG	GACAGTCTGA	AGAAATCCTG	CCAGGACTGT	1560
AAGTTGCAGG	CTGACGACCA	TCGAGATCCC	GGCGGGAATG	GAGGGAATGG	AGCAGAGACA	1620
GCCGAGGACA	GTAGAGTCCA	GGAAGTGGAG	AGTCAGGTGA	ACAAGCTGTC	CTCAGAGCTG	1680
AAGAATGCAA	AGGACCAGAT	CCAGGGGCTG	CAGGGGCGCC	TGGAGACGCT	CCATCTGGTA	1740
AATATGAACA	ACATTGAGAA	CTACGTGGAC	AACAAAGTGG	CAAATCTAAC	CGTTGTGGTC	1800
AACAGTTTGG	ATGGCAAGTG	TTCCAAGTGT	CCCAGCCAAG	AACACATGCA	GTCACAGCCG	1860
GGTAGGTGTA	ATGAGGGTCA	TACAGTTTGT	TCATGAAAGC	TGTATAGCCA	GATAGTGGCC	1920
ATAAACATTA	ACCCGAGGGA	GCATAAGTTA	GTCAGACTTT	CACCTGTTAA	GTTATGGCAG	1980
GAGAAACAAG	TGTTTTCTCA	AATGAGACAA	CAGAAATGGT	AAATGATCCA	CGTACAAAAA	2040
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GTCGACCAAC	AGACGAGCAG	AAACAGATTC	CTCCCGGAAT	CTGAACACAT	ATTTGAACAC	2160
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CAAGCTGGCC	GTGATATCCA	CGTCGTAAGG	CTGCTGTGTG	GGTTCAGTGA	AAACTGTTAC	3480
AGTGATTGGC	AGAGTTTCTG	GAGGTCATTG	ACCCTCATTA	AACCTTGCAT	ACACTTATTC	3540
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 CACACTGGTT TATATTTTGA AAGCCAATCC TAATCCCAAA GCAATACTGT TGTCGAGGAG 5340  
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## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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 20 25 30  
 Ser Ala Gln Ala Ala Cys Pro Ala Arg Leu Glu Gly Ser Gly Arg Cys  
 35 40 45  
 Glu Gly Ser Gln Cys Pro Phe Gln Leu Thr Leu Pro Thr Leu Thr Ile  
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 Gln Leu Pro Arg Gln Leu Gly Ser Met Glu Glu Val Leu Lys Glu Val  
 55 70 75 80



Arg Thr Leu Lys Glu Ala Val Asp Ser Leu Lys Lys Ser Cys Gln. Asp  
 85 90 95  
 Cys Lys Leu Gln Ala Asp Asp His Arg Asp Pro Gly Gly Asn Gly Gly  
 100 105 110  
 Asn Gly Ala Glu Thr Ala Glu Asp Ser Arg Val Gln Glu Leu Glu Ser  
 115 120 125  
 Gln Val Asn Lys Leu Ser Ser Glu Leu Lys Asn Ala Lys Asp Gln Ile  
 130 135 140  
 Gln Gly Leu Gln Gly Arg Leu Glu Thr Leu His Leu Val Asn Met Asn  
 145 150 155 160  
 Asn Ile Glu Asn Tyr Val Asp Asn Lys Val Ala Asn Leu Thr Val Val  
 165 170 175  
 Val Asn Ser Leu Asp Gly Lys Cys Ser Lys Cys Pro Ser Gln Glu His  
 180 185 190  
 Met Gln Ser Gln Pro Val Gln His Leu Ile Tyr Lys Asp Cys Ser Asp  
 195 200 205  
 His Tyr Val Leu Gly Arg Arg Ser Ser Gly Ala Tyr Arg Val Thr Pro  
 210 215 220  
 Asp His Arg Asn Ser Ser Phe Glu Val Tyr Cys Asp Met Glu Thr Met  
 225 230 235 240  
 Gly Gly Gly Trp Thr Val Leu Gln Ala Arg Leu Asp Gly Ser Thr Asn  
 245 250 255  
 Phe Thr Arg Glu Trp Lys Asp Tyr Lys Ala Gly Phe Gly Asn Leu Glu  
 260 265 270  
 Arg Glu Phe Trp Leu Gly Asn Asp Lys Ile His Leu Leu Thr Lys Ser  
 275 280 285  
 Lys Glu Met Ile Leu Arg Ile Asp Leu Glu Asp Phe Asn Gly Leu Thr  
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 Asp Arg Asp Asn Asp Arg Tyr Pro Ser Gly Asn Cys Gly Leu Tyr Tyr  
 355 360 365  
 Ser Ser Gly Trp Trp Phe Asp Ser Cys Leu Ser Ala Asn Leu Asn Gly  
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 405 410 415  
 Ser Phe Lys Gln Ala Lys Met Met Ile Arg Pro Lys Asn Phe Lys Pro  
 420 425 430

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07/12/01

## <120> Methods of Modulating Immune Coagulation

<130> 9579-37

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